

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:13:06 ; Search time 101.54 Seconds
(without alignments)
48.262 Million cell updates/sec

Title: US-09-052-089a-6
Perfect score: 293
Sequence: 1 LSLCTICSDFFDHSRDVAAL.....IOWFETAPSRTPCPCRIQVG 51

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	244	83.3	433	2 T30807	TRAF interacting p
2	127	43.3	310	2 C84701	hypothetical prote
3	125	42.7	325	2 F86321	F6A14.12 protein -
4	123	42.0	158	2 T13738	hypothetical prote
5	113	38.6	224	2 E86321	hypothetical prote
6	112	38.2	344	2 T05064	hypothetical prote
7	112	38.2	383	2 A86315	F2H15.19 protein -
8	110	37.5	274	2 T48296	hypothetical prote
9	108	36.9	489	2 T26069	hypothetical prote
10	107	36.5	137	2 T46904	hypothetical prote
11	107	36.5	551	2 S66695	probable membrane
12	106.5	36.3	506	2 F85016	probable RING zinc
13	106	36.2	367	2 H96764	protein RING zinc
14	106	36.2	425	2 T25457	hypothetical prote
15	106	36.2	524	2 F96572	protein F12M16.10
16	105	35.8	1238	2 T15919	hypothetical prote
17	104.5	35.7	441	2 F71425	hypothetical prote
18	104	35.5	351	2 F96597	hypothetical prote
19	102.5	35.0	237	2 G84678	probable RING zinc
20	102	34.8	180	2 T51859	probable RING zinc
21	102	34.8	292	2 T06684	hypothetical prote
22	101.5	34.6	425	2 A84849	probable RING zinc
23	100.5	34.3	157	2 T13027	RING-H2 finger pro
24	100.5	34.3	157	2 T51841	RING-H2 finger pro
25	99.5	34.0	206	2 C85067	hypothetical prote
26	99.5	34.0	1610	2 T11681	hypothetical prote
27	98.5	33.6	227	2 T00428	hypothetical prote
28	98	33.4	204	2 G84530	probable RING-H2 z
29	98	33.4	324	2 E84918	hypothetical prote

30	98	33.4	343	2 H96703	probable RING zinc
31	97.5	33.3	257	2 T48058	RING-H2 zinc finger
32	97	33.1	211	2 F86488	protein T32E20.33
33	97	33.1	235	2 T19328	hypothetical prote
34	97	33.1	407	2 G96835	hypothetical prote
35	96.5	32.9	194	2 C85130	probable RING zinc
36	96.5	32.9	203	2 T48129	hypothetical prote
37	96.5	32.9	304	2 T52079	probable RING zinc
38	96.5	32.9	408	2 T25524	hypothetical prote
39	96	32.8	145	2 B96705	unknown protein, 8
40	96	32.8	377	2 T26958	hypothetical prote
41	96	32.8	488	2 T10675	hypothetical prote
42	96	32.8	530	2 T50499	hypothetical prote
43	95.5	32.6	162	2 E84455	probable RING zinc
44	95	32.4	189	2 T05383	hypothetical prote
45	95	32.4	238	2 T49155	hypothetical prote

ALIGNMENTS

RESULT 1
T30807
TRAF interacting protein - Fugu rubripes
C:Species: Fugu rubripes
C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T30807
R:Cottage, A.J.; Clark, M.; Hawker, K.; Umrantia, Y.; Wheller, D.; Bishop, M.; Elgar, F.E.S. Lett. 443, 370-374, 1999
A:Title: Three receptor genes for plasmalogen related growth factors in the genome of F.E.S. Lett. 443, 370-374, 1999
A:Reference number: Z20880; MUID:99148833
A:Accession: T30807
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-433 <COT>
A:Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA09084.1
C:Genetics:
A:Gene: TRIP
A:Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3

Query Match 83.3%; Score 244; DB 2; Length 433;
Best Local Similarity 83.0%; Pred. No. 2e-21;
Matches 39; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTICSDFFDHSRDVAALHCGHTFHLLQCLIQWFETAPSRTPCPCRIQV 50
|||||
Db 7 CTICSDFFDHSRDVAALHCGHTFHLLQCLIQWFETAPSRTPCPCRIQV 53

RESULT 2
C84701
hypothetical protein At2g29840 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84701
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: C84701
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <STO>
A:Cross-references: GB:AE002093; NID:g3582320; PIDN:AAC35217.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g29840
A:Map position: 2

Query Match 43.3%; Score 127; DB 2; Length 310;

Best Local Similarity 41.7%; Pred. No. 1,1e-07;
Matches 20; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

OY 3 LCITCSDFDHSRDVAALHCGHTFHLOCLIQWETAPSRCPQCRIOY 50
Db 260 MCSICLDFDGRSIVALLPCGHEFDDECAIKWFET--NHDCPLCRFKL 305

RESULT 3

F6A14.12

hypothetical protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001

C:Accession: F86321

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: F86321

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1325 <STO>

A:Cross-references: GB:AE005172; NID:g6730707; PIDN:AAF27102.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 42.7%; Score 125; DB 2; Length 325;
Best Local Similarity 39.6%; Pred. No. 2e-07;
Matches 19; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

OY 3 LCITCSDFDHSRDVAALHCGHTFHLOCLIQWETAPSRCPQCRIOY 50
Db 276 VCTICLEFDDGRSIVALLPCGHEFDDECAIKWF--VSHVCPCLRLEL 321

RESULT 4

T13738

hypothetical protein 22E5.12 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13738

R:Murphy, L.; Harris, D.; Barrell, B.

submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: Z17668

A:Accession: T13738

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <MUR>

A:Cross-references: EMBL:AL031765; NID:el371523; PID:el326038; PIDN:CAB41708.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0000667

A:Intons: 41/2

A>Note: EG:22E5.12

C:Superfamily: RING finger homology

F:4-54/Domain: RING finger homology <RRN>

Query Match 42.0%; Score 123; DB 2; Length 158;
Best Local Similarity 51.1%; Pred. No. 1.9e-07;
Matches 24; Conservative 4; Mismatches 17; Indels 2; Gaps 1;

OY 3 LCITCSDFDHSRDVAALHCGHTFHLOCLIQWETAPSRCPQCRIOY 49
Db 7 ICTICSERFRTSDNIQSGHAFHEDELDHM--RKOSRTCPICRSQ 51

RESULT 5

E86321

hypothetical protein F6A14.13 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: E86321

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: E86321

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1224 <STO>

A:Cross-references: GB:AE005172; NID:g6730708; PIDN:AAF27103.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 38.6%; Score 113; DB 2; Length 224;
Best Local Similarity 40.4%; Pred. No. 3.9e-06;
Matches 19; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAALHCGHTFHLOCLIQWETAPSRCPQCRIOY 50
Db 175 CTICLDFDGRSIVALLPCGHEFDDECAIKWFET--NHDCPLCRFKL 219

RESULT 6

T05064

hypothetical protein M3E9.170 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000

C:Accession: T05064

R:Bevan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hohelsel, J.; Mewes, H.W.; Ma

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z15396

A:Accession: T05064

A:Molecule type: DNA

A:Residues: 1-344 <BEV>

A:Cross-references: EMBL:AL022223

A:Experimental source: cultivar Columbia; BAC clone M3E9

C:Genetics:

A:Map position: 4

A>Note: M3E9.170

C:Superfamily: RING finger homology

F:225-275/Domain: RING finger homology <RRN>

Query Match 38.2%; Score 112; DB 2; Length 344;
Best Local Similarity 38.3%; Pred. No. 7.3e-06;
Matches 18; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAALHCGHTFHLOCLIQWETAPSRCPQCRIOY 50
Db 229 CSICLDFFDKGSEAKEMPKHFKHICVPLWLEHSS--CPVCRYEL 273

RESULT 7

A86315

F2H15.19 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001

C:Accession: A86315

R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso
Chili, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Hultzar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: A86141; MUID:21016719

A:Accession: A86315

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-383 <5M0>

A:Cross-references: GB:AE005172; NID:99665074; PIDN:AA97276.1; GSPDB:GN00141

C:Genetics:

C:Map position: 1

Query Match	38.2%	Score 112	DB 2	Length 383
Best Local Similarity	36.4%	Pred. No. 8e-06		
Matches	16	Conservative	11	Mismatches 15; Indels 2; Gaps 1
QY	4	CTICSDFDHSDVAIHGHTFHQCLQWETAPSRCPQCR	47	
DB	335	LTICDDEDEVELNGSHFHVCKQWL--SRKNAPVCK	376	

RESULT 8
T48296
hypochemical protein F9G14.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T48296
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysseart, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z2491
A:Accession: T48296
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <BEV>
A:Cross-references: EMBL:AL162973
A:Experimental source: cultivar Columbia; BAC clone F9G14
C:Genetics:
A:Map position: 5
A:Note: F9G14.60
C:Superfamily: RING finger homology
f: 201-251/Domain: RING finger homology <RRN>

Query Match 37.5%; Score 110; DB 2; Length 274;
 Best Local Similarity 38.3%; Pred. No. 1e-05;
 Matches 18; Conservative 7; Mismatches 20; Indels 2; Gaps 1

```

RESULT      9
T26069
hypothetical protein W02A11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T26069
R:White, S.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20147
A:Accession: T26069
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

```

A:Residues: 1-489 <MIL>
A:Cross-references: EMBL:Z82062; PIRDB:CA804890.1; GSPDB:GN00019; CESP:W02A11.3
A:Experimental source: clone W02A11
C:Genetics:
A:Gene: CESP:W02A11..3
A:Map position: 1
A:Introns: 58/3; 129/3; 361/3; 444/3
A:Superfamily: RING Finger homology
A:429-479/Domain:RING Finger homology <RRN>

36.9%; Score 108; DB 2; Length 489;
 Best Local Similarity 29.8%; Pred. No. 2.9e-05;
 Matches 14; Conservative 12; Mismatches 19; Indels 2; Gaps 1;

RESULT 10
T46904
hypothetical protein DKFzp761D081.1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
C:Accession: T46904
R:Ottewaeldey, B.; Obermaier, B.; Mewes, H.W.; Well, B.; Wiemann, S.
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24136
A:Accession: T46904
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <AAA>
A:Cross-references: EMBL:AL157474
A:Experimental source: adult amygdala; clone DKFzp761D081
C:Genetic:
A:Note: DKFzp761D081.1
C:Superfamily: RING finger homology
;81-131/Domain: RING finger homology <RRN>

Query Match	36.5%	Score 107	DB 2	Length 137
Best Local Similarity	38.3%	Pred. No. 1.3e-05		
Matches	18	Conservative	7	Mismatches 20; Indels 2; Gaps 1
QY	4	CTICSDFFDHSRDVAIHCGHTFHLCCLIQWETAPSRFCPOCRIOV	50	
Db	85	CTICSTILEEGDVRRLPCMHLEHVCVDQWILT--NKKCPICRVDI	129	

RESULT 11

S66695
probable membrane protein YOL013c - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein O2341

C:Species: *Saccharomyces cerevisiae*

C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 02-Sep-2000

C:Accession: S66695

R:Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996

A:Reference number: S66685

A:Accession: S66695

A:Molecule type: DNA

A:Residues: 1-951 <HUG>

A:Cross-references: EMBL:Z74755; NID:q1419784; PID:e522259; PID:q1419785; MIPS:YOL013

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:HRP1

A:Cross-references: SGD:S0005373; MIPS:YOL013c

A:Map position: 15L

C:Superfamily: RING finger homology

C:Keywords: transmembrane protein

C:10-26/Domain: transmembrane #status predicted <TM1>

C:46-62/Domain: transmembrane #status predicted <TM2>

```
F:105-12/Domain: transmembrane #status predicted <TM3>
F:144-160/Domain: transmembrane #status predicted <TM4>
F:185-201/Domain: transmembrane #status predicted <TM5>
F:345-405/Domain: RING finger homology <RRN>
```

Query Match	36.5%;	Score 107;	DB 2;	Length 551;
Best Local Similarity	37.3%;	Pred. No. 4.3e-05;		
Matches	22;	Conservative	6;	Mismatches 19;
			Indels	12;
			Gaps	2;

QY 2 SLCTICSDFFHDS-----RDVAALHCCHTFHLQCLIOFETAPBRTCPQCRIV 50
::||| | : ||| | | :||| |
Db 347 NICLICMDELHSPNQQTWKNKNNKKPKRLPCGHILHLSCLKNMNER--SQTCPICRLPV 403

```

RESULT 12
F85016
probable RING zinc finger protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence-revision 16-Feb-2001 #text-change 16-Feb-2001
C:Accession: F85016
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory Press, 1999
Nature 402, 769-777, 1999
Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

```

A:Status: preliminary
A:Accession: 15938
A:Molecule type: DNA
A:Residues: 1506 <Str>
A:Cross-references: GB:NC_001268; NID:97267624; PIDN: CAB80936.1; GSFDF:GN00140
C:Genetics:
A:Gene: ATAg01270
A:Map position: 4

Query Match	36.3%	Score 106.5;	DB 2;	Length 506;
Best Local Similarity	39.6%	Pred. No. 4.5e-05;		
Matches	21;	Conservative	10;	Mismatches 13;
			Indels	9;
			Gaps	3

```

Oy      2 SLCTICSD----FFDHSRDVAIHCGTFLHQLLIQWFFETAPS--RTCPQCR 47
          ::::| | | | | | | | | | | | | | | | | | | | | | | | | |
Db     10 AICSICEDLKPVENTLQISIA--CGHVFEHLCLQWFEYCSTINKRNPICK 60

```

RESULT 13
H96764
protein RING zinc finger protein P25P22.18 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

R.T.: Theologian, D. Eckert, M.K.: J. Palm, C.J.: Federici, N.A.: Kaul, S.: White, O.: Alonso, C.: Chiu, C.W.: Chung, M.J.: Conn, L.: Conway, A.B.: Conway, A.R.: Cressy, T.H.: Dewar, K.: Hansen, N.F.: Hughes, B.: Hutzar, L. Nature 408, 816-820, 2000

A: Authors: Hunter, J.L.: Jenkins, J.: Johnson-Hopson, C.: Khan, S.: Khaykin, E.: Kim, C.C.A.: Li, J.H.: Li, Y.: Liu, X.: Liu, S.X.: Liu, Z.A.: Lucas, J.S.: Malt, R.: Marzall, Rizzo, M.: Rooney, T.: Rowley, D.: Sakano, H. A: Authors: Salberg, S.L.: Schwartz, J.R.: Shinn, P.: Southwick, A.M.: Sun, H.: Tallon, Kert, M.: Wu, D.: Yu, G.: Fraser, C.M.: Venter, J.C.: Davis, R.W.

A:Reference number: H96764, MOLID:Z1010715
A:Accession: H96764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-367 <STPO>
A:Cross-references: GB:AE005173; NID:g6662739; PIDN:AAF24845.1; GSSTDB:GN001411
C:Genetics:
A:Gene: F25P22.18
A:Map position: 1

Query Match	36.28;	Score 106;	DB 2;	Length 367;
Best Local Similarity	36.48;	Pred. No. 4e-05;		

	Matches	16;	Conservative	8;	Mismatches	16;	Indels	2;	Gaps	1
QY	4	CTICSD	FPDHSRDVA	AIHCGHTFHLQCLQ	METAPSR	CKPCOR	47			
			:	:		:				
			:	:		:				
Db	319	CTICD	DEYAKDEVEL	RCGHRFHIDCVQML	--VRKN	CSPPCK	360			

RESULT 14
T25457
hypothetical protein B0432.9 - *Caenorhabditis elegans*

C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C; Accession: T23457
R; Henkhaus, J.; Mohlmann, P.
submitted to the EMBL data Library, December 1996
A; Description: The sequence of C. elegans cosmid B0432.
A; Accession number: F20020

A:Accession:J25457
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-425 <HEN>
A:Cross-references: EMBL:U08036; PIDN:AB37893.1; GSPDB:GN00020; CESP:B0432.9
A:Experimental source: strain Bristol NZ; clone B0432
C:Genetics:
A:Gene: CESP:B0432.9
A:Map position: 2
A:Introns: 64/3; 99/3; 165/1; 267/3; 350/2; 386/2
C:Superfamily: RING finger homology
I:188-238/Domain: RING finger homology <RRN>

Query Match	36.2%;	Score 106;	DB 2;	Length 425;
Best Local Similarity	40.9%;	Pred. No. 4.5e-05;		
Matches 18;	Conservative 7;	Mismatches 17;	Indels 2;	Gaps 1.

QY 4 CTICSDFFDHSRDVAAIHCGETHFLQCLIQWETAPSRTPCPCR 47
|::| : ::||| | : ||| |
Db 192 CSICFEDLKQNDKISAIVCGHYHHGCSIQMIAT--KRQCPSCR 23

RESULT 15
F96572
protein F12M16.10 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
!Accession: F96572

R:Theologian, A. Ecker, J.R.: Palm, C.J.: Federpiel, N.A.: Kaul, S.: White, O.: Alvarado, C.M.: Chung, M.K.: Conn, L.: Conway, A.B.: Conway, A.R.: Cressy, T.H.: Dettar, N.E.: Hughes, B.: Hutzler, L.
Nature 408, 815-820, 2000

A:Authors: Hunter, J.L., Jenkins, J., Johnson-Hopson, C., Khan, S., Khaykin, E., Kim, C.A., Li, J.H., Li, T., Lin, X., Liu, S.X., Liu, Z.A., Luros, J.S., Maitli, R., Marziani, Rizzo, M., Rooney, T., Rowley, D., Sakano, H.
A:Authors: Salzberg, S.L., Schwartz, J.R., Shinn, P., Southwick, A.M., Sun, H., Tallon, K., M., Wu, D., Yu, G., Fraser, C.M., Venter, J.C.: Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
Reference number: A86141: MUID:21016719

A:Accession: F50572
A:Status: Preliminary
A:Molecule_type: DNA
A:Residues: 11524 <STO>
A:Cross_references: GB:AE005173; NID:q7769853; PIDN:AAE69531.1; GSPDB:GN001411
C:Genetics:
A:Gene: F12M16.10
A:Map position: 1

Query Match	36.2%	Score 106	DB 2	Length 524
Best Local Similarity	36.4%	Pred. No. 5.4e-05		
Matches 16: Conservative	8;	Mismatches 18;	Indels 2;	Gaps 1;
4 CTCGDFDHSRDVAIHGCHFFHLQCLLOMFETAPSRTPPCR	47			
: : : : : :				

Db 472 CTICQSFNKEKIALDLDCGHEYHAECLERKL--IVKNVCPICK 513

RESULT 16

hypotheetical protein EEBD8.9 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000

C:Accession: T15919

R:Chisoe, S.

submitted to the EMBL Data Library, July 1995

A:Description: The sequence of C. elegans cosmid EEBD8.

A:Reference number: Z18428

A:Accession: T15919

A:Status: preliminary; translated from GB/EMBL/DDbJ

A:Molecule type: DNA

A:Residues: 11238 <CHT>

A:Cross-references: EMBL:023484; NID:g733597; PID:g733606; PIDN:MAC46769.1; CESP:EEBD8.9

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:EEBD8.9

A:Introns: 16/3; 60/3; 140/1; 192/3; 269/2; 402/2; 637/3; 717/3; 769/1; 855/3; 888/3; 10

C:Superfamily: RING finger homology

F:904-950/Domain: RING finger homology <RRN>

Query Match 35.8%; Score 105; DB 2; Length 1238;

Best Local Similarity 44.7%; Pred. No. 0.00015;

Matches 21; Conservative 5; Mismatches 15; Indels 6; Gaps 2;

Qy 1 LSLCTICSDFFDHSRDVAIHCGRTHLQCLIQWFTAPSRCPQCR 47

Db 905 LPTCAVCLERMDSS-VLAILCNHSPHARCLEQWAD----NTCVR 945

RESULT 17

F71425

hypotheetical protein - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cross)

A:Variety: Columbia

C>Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 02-Sep-2000

C:Accession: F71425

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk

P.; Medler, H.; Medler, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Scheffter, M.; Funk, B.

Nature 391, 485-486, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech

erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palmer, K.; Benes, V.; Reichen, S.; Ans

C.; Chalwatzi, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thal*

A:Reference number: A71400; MUID:98121113

A:Accession: F71425

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-441 <BEV>

A:Cross-references: GB:297340; NID:g2244950; PID:e326963; PID:g2244955

C:Genetics:

A:Map position: 4COP9-4G3845

C:Superfamily: RING finger homology

F:278-329/Domain: RING finger homology <RRN>

Query Match 35.7%; Score 104.5; DB 2; Length 441;

Best Local Similarity 39.6%; Pred. No. 7e-05;

Matches 19; Conservative 9; Mismatches 17; Indels 3; Gaps 2;

Qy 4 CTICSDFFDHSRDVAIHCGRTHLQCLIQWFTAPSRCPQCR 50

Db 282 CSVCLSEFKDNESGRVMPNCKHTFHVCIDMWFHSHS--CPICRSQI 327

RESULT 18

F96597

hypotheetical protein T5A14.7 [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: F96597

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Matzla

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: A86141; MUID:21016719

A:Accession: F96597

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-351 <STO>

A:Cross-references: GB:AE005173; NID:g4204263; PIDN:AAD10644.1; GSPDB:GN00141

C:Genetics:

A:Gene: T5A14.7

A:Map position: 1

Query Match 35.5%; Score 104; DB 2; Length 351;

Best Local Similarity 38.3%; Pred. No. 6.6e-05;

Matches 18; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

Qy 4 CTICSDFFDHSRDVAIHCGRTHLQCLIQWFTAPSRCPQCR 50

Db 223 CSVCLDFEIGTEAKIKMPCRHKFSDDLPLMLHSS--CPVRYQL 267

RESULT 19

G84678

probable RING zinc finger protein [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cross)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: G84678

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

euser, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: A84420; MUID:2083487

A:Accession: G84678

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 <STO>

A:Cross-references: GB:AE002093; NID:g4510422; PIDN:AAD21508.1; GSPDB:GN00139

C:Genetics:

A:Gene: AT2927940

A:Map position: 2

Query Match 35.0%; Score 102.5; DB 2; Length 237;

Best Local Similarity 42.2%; Pred. No. 7.1e-05;

Matches 19; Conservative 4; Mismatches 19; Indels 3; Gaps 2;

Qy 4 CTICSDFFDHSRDVAIHCGRTHLQCLIQWFTAPSRCPQCR 47

Db 140 CVICLDFEIGTEAKIKMPCRHKFSDDLPLMLHSS--TCPICR 182

RESULT 20

T51859

RING-H2 finger protein RHG2 [imported] - *Arabidopsis thaliana* (fragment)

C:Species: *Arabidopsis thaliana* (mouse-ear cross)

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C:Accession: T51859

R:Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K.

FEBS Lett. 436, 283-7, 1998

A:Title: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the
 A:Reference number: Z13771; MUID:98452556
 A:Accession: T51859
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-190 <JEN>
 A:Cross-references: EMBL:AF071813; PIDN:AAC69857.1

	Query Match	Score 102;	DB 2;	Length 190;
	Best Local Similarity	31.8%;	Pred. No. 6.7e-05;	
Matches	14; Conservative	9;	Mismatches 19;	Indels 2;
	Gaps	1;		
OY	4 CTICSDPFDHSDVAALHGCTFTHLQCLIQMETAPSRFCPOOR	47		
	: : : : : : : : : : : : :			
Dd	136 CCVCQEETEGEDMGTLECGNEHFHSQCILEEWLK--OKNLCPPTCK	177		

RESULT 21
T06684
hypothetical protein T17F15.140 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000
C:Accession: T06684
R:Quellier, F.; Choinse, N.; Robert, C.; Brottier, P.; Wincker, P.; Catolico, L.; Artig
submitted to the Protein Sequence Database, April 1999
A:Accession: T06684
A:Reference number: 215793
A:Molecule type: DNA
A:Residues: 1-292 <CDS>
A:Cross-references: EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.140
A:Experimental source: cultivar Columbia; BAC clone T17F15
A:Genetics:
A:Gene: ATSP:T17F15.140
A:Map position: 3
A:Introns: 37/3: 68/3: 90/3: 143/3: 181/3
C:Superfamily: RING finger homology
P:165-215/Domain: RING finger homology <RRN>

Query March 34.8%; score 102; DB 2; length 292;
Best Local Similarity 36.2%; Pred. No. 9,7e-05;
Matches 17; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAIHCGHTFHLQCLLIQMFETAPSRFCPOCRIOV 50
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 169 CLICEEFHIGHEVEGLPCAHNFHCICIDWLRL--NVKCPRCRCSV 213

RESULT 22

A84849
Probable RING zinc finger protein [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84849

R:Llin,X.; Kaul,S.; Rounsley,S.D.; Shea,T.P.; Benito,M.I.; Town,C.D.; Fujii,C.Y.;
M.; Koo,H.; Moffit,K.S.; Cronin,L.A.; Shen,M.; VanNaken,S.E.; Umayam,L.; Tallon,L.
euss,D.; Nierman,W.C.; White,O.; Eisen,J.A.; Salzberg,S.L.; Fraser,C.M.; Venter,
J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487

A:Accession: A84849

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-425 <STO>

A:Cross-references: GB:AE002093; NID:g1871181; PID:AAB63541.1; GSPPDB:GN00139

C:Genetics:

A:Gene: Atg42030

A:Map position: 2

Query Match	34.68;	Score 101.5;	DB 2;	Length 425;
Best Local Similarity	36.28;	Pred. No. 0.00015;		

	Matches	17, Conservative	9, Mismatches	18, Indels	3, Gaps	1, Ambiguous
QY	4	CTICSDFDHSDVAIHCGHTFHQCLQLQWETAPSRCTPCRCIQV	50			
Db	141	CTICIDL---SKDPVVTNGHLYCMSCLYQWLVQVSEAKCPCKSEV	184			

```

RESULT 23
T13027
RING-H2 finger protein RHA1b - Arabidopsis thaliana
N:Alternate names: protein F8L21.150
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 02-Sep-2000
C:Accession: T13027
R:Bayan, M.; Peters, S.A.; van Staveren, M.; Dirse, W.; Stiekema, W.; Bancroft, I.,
submitted to the Protein Sequence Database, July 1999
A:Reference number: 217587
A:Accession: T13027
A:Molecule type: DNA
A:Residues: 1-157 <BEV>
A:Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.150
A:Experimental source: cultivar Columbia; BAC clone F8L21
C:Genetics:
A:Gene: ATSP:F8L21.150
A:Map position: 4
C:Superfamily: RING finger homology
;81-134/Domain: RING finger homology <RRN>

```

	Query Match	34.3%	Score 100.5:	DB 2:	Length 157;
	Best Local Similarity	42.2%	Pred. No. 8.6e-05;		
	Matches 19; Conservative	4;	Mismatches 21;	Indels 1;	Gaps 1;
OY	4 CTIC-SDFEDHSRDVAIAIHCGTFHLOCIOMFEAPSPCTCPCR	47			
	:	: :			
Db	85 CTCVCSDEVSODKIRQLPRCGVHFHHRCIDRAIVLONCKITCCIC	129			

RESULT 24
T51841
RING-H2 finger protein RHAB [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C/Accession: T51841
R/Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K.
FEBS Lett. 436, 283-7, 1998
A>Title: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the
A/Reference number: Z13771; MUID:98452956
A/Accession: T51841
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-157 <JEN>
A/Cross-references: EMBL:AF078821; PIDN:AAC68670.1
A/Experimental source: cultivar Columbia

Query Match	34.3%	Score 100.5	DB 2	Length 157
Best Local Similarity	42.2%	Pred. No. 8,6e-05		
Matches 19	Conservative 4	Mismatches 21	Indels 1	Gaps 1
OY	4	CTTC-SDFEDHSRDVAAITHCGHTPLQCLLIOWFEAPSRTCQCR	47	
	11	11	11	11
	11	11	11	11
Db	85	CTVCLSDFVSDSKIRQLRPCKGVHNRLLDRNIVDCKNITPICR	129	

RESULT 25
C85067
hypothetical protein ATr4g05350 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C:Accession: C85067
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory Press, New York, NY, USA, 1999
Feature 402, 769-777, 1999

A:Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
 A:Reference number: A85001; MUID:20083488
 A:Accession: G85067
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-206 <STO>
 A:Cross-references: GB:NC_001268; NID:g7267295; PIDN:CA81077.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: AT4G05350
 A:Map position: 4
 C:Superfamily: *Arabidopsis thaliana* hypothetical RING finger protein F16J13.210; RING fi

Query Match 34.0%; Score 99.5; DB 2; Length 206;
 Best Local Similarity 36.0%; Pred. No. 0.00014;
 Matches 18; Conservative 8; Mismatches 19; Indels 5; Gaps 2;

OY 4 CTICSDFF---DHSRDVAIHCGHTFHLOCLIQWETAPSRTPCQRIQV 50
 T11681
 Db 157 CSICLESIVSGPKPRDVTBMTCSHFHNGCLLEWLKR--KNTCPICRTEI 204

RESULT 26
 T11681
 hypothetical protein SPBC21D10.09c - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: *Schizosaccharomyces pombe*
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
 C:Accession: T11681
 R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 Submitted to the EMBL Data Library, September 1998
 A:Reference number: 217313
 A:Accession: T11681
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1610 <SEE>
 A:Cross-references: EMBL:AL031536; NID:el319499; PID:el319508
 A:Experimental source: strain 972h(-)
 C:Genetics:
 A:Map position: IIR
 A:Introns: 10/2
 A:Note: SPBC21D10.09c
 C:Superfamily: RING finger homology
 F:1554-1609/Domain: RING finger homology <RRN>

Query Match 34.0%; Score 99.5; DB 2; Length 1610;
 Best Local Similarity 38.3%; Pred. No. 0.00062;
 Matches 18; Conservative 5; Mismatches 21; Indels 3; Gaps 1;

OY 4 CTICSDFFDHSRDVAIHCG---HTFHLOCLIQWETAPSRTPCQRIQV 47
 Db 1558 CAICYSIVSYVERITLPNKRCCGICRKHFAASCLYKFKSSNSRCPICR 1604

RESULT 27
 T00428
 hypothetical protein At2g47560 [imported] - *Arabidopsis thaliana*
 N:Alternate names: hypothetical protein T30B22.14
 C:Species: *Arabidopsis thaliana* (mouse-ear cross)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
 C:Accession: T00428; G84916
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc
 submitted to the EMBL Data Library, October 1998
 A:Description: *Arabidopsis thaliana* chromosome II BAC T30B22 genomic sequence.
 A:Reference number: 214149
 A:Accession: T00428
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-227 <ROU>
 A:Cross-references: EMBL:AC002535; NID:g2529657; PID:g2529671
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487
 A:Accession: G84916
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-227 <STO>
 A:Cross-references: GB:AE002093; NID:g2529671; PIDN:AAC62854.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: T30B22.14; At2g47560
 A:Map position: 2
 C:Superfamily: *Arabidopsis* hypothetical protein F19I3.22; RING finger homology
 F:104-155/Domain: RING finger homology <RRN>

Query Match 33.6%; Score 98.5; DB 2; Length 227;
 Best Local Similarity 37.5%; Pred. No. 0.0002;
 Matches 18; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

OY 4 CTIC-SDFFDHSRDVAIHCGHTFHLOCLIQWETAPSRTPCQRIQV 50
 Db 108 CSVCLSEFEEDRGRLPKCGSHFVDCIDTFPRS--RSTCPICRAVY 153

RESULT 28
 G84530
 probable RING-H2 zinc finger protein [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cross)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84530
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487
 A:Accession: G84530
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-204 <STO>
 A:Cross-references: GB:AE002093; NID:g4335724; PIDN:AAD17402.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g15580
 A:Map position: 2

Query Match 33.4%; Score 98; DB 2; Length 204;
 Best Local Similarity 36.2%; Pred. No. 0.00021;
 Matches 17; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAIHCGHTFHLOCLIQWETAPSRTPCQRIQV 50
 Db 158 CAICLDREKKGKGTLVHLPICAKHFSICILPWLDT--NVYCPYCRDTI 202

RESULT 29
 E84918
 hypothetical protein At2g47700 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cross)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: E84918
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487
 A:Accession: E84918
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-324 <STO>
 A:Cross-references: GB:AE002093; NID:g3738284; PIDN:AAC63626.1; GSPDB:GN00139

C:Genetics:
A:Gene: At2g47700
A:Map position: 2

Query Match 33.4%; Score 98; DB 2; Length 324;
Best Local Similarity 41.3%; Pred. No. 0.00032;
Matches 19; Conservative 5; Mismatches 20; Indels 2; Gaps 1;

OY 4 CTIC--SDFPDHSDVAAIHCGHTFHLOCLIQWFTAPSRPCPCR 47
Db 38 CSICLESYLDGTRSKATLQCGHFDLCIGSAFNMKGAMQCPNCR 83

RESULT 30
H96703
probable RING zinc finger protein T23K23.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96703
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
anssen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H96703
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-343 <STO>
A:Cross-references: GB:AE005173; NID:96553889; PIDN:AAF16555.1; GSPDB:GN00141
C:Genetics:
A:Gene: T23K23.8
A:Map position: 1

Query Match 33.4%; Score 98; DB 2; Length 343;
Best Local Similarity 27.7%; Pred. No. 0.00033;
Matches 13; Conservative 13; Mismatches 19; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAAIHCGHTFHLOCLIQWFTAPSRPCPCR 50
Db 292 CCICLSTYEDGAEIVSLPCNHHSCTIVKWLKM--NATCPLCKFNI 336

RESULT 31
T48058
RING-H2 zinc finger protein ARI5 - Arabidopsis thaliana
N:Alternate names: protein P26K9.120
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Dec-2000
C:Accession: T48058
R:Bloeker, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quetler, F.; Salanoubat,
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24465
A:Accession: T48058
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <BLO>
A:Cross-references: EMBL:AL162651
A:Experimental source: cultivar Columbia; BAC clone P26K9
C:Genetics:
A:Map position: 3
A:Gene: P26K9.120
C:Superfamily: Arabidopsis hypothetical protein F19I3.22; RING finger homology
F:109-160/Domain: RING finger homology <RRN>

Query Match 33.3%; Score 97.5; DB 2; Length 257;
Best Local Similarity 37.3%; Pred. No. 0.0003;
Matches 19; Conservative 7; Mismatches 22; Indels 3; Gaps 2;

OY 1 LSLCTIC--SDFPDHSDVAAIHCGHTFHLOCLIQWFTAPSRPCPCR 50
Db 110 LECCSVCLSEFEEDDEGRVLPKCGHVFHVCIDYWFRRSS--CPLCRAPV 158

RESULT 32
F86488
protein T32E20.33 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F86488
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
anssen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F86488
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <STO>
A:Cross-references: GB:AE005172; NID:98778785; PIDN:AAF79793.1; GSPDB:GN00141
C:Genetics:
A:Gene: T32E20.33
A:Map position: 1

Query Match 33.1%; Score 97; DB 2; Length 211;
Best Local Similarity 35.6%; Pred. No. 0.00029;
Matches 16; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

OY 3 LCTICSDFFDHSRDVAAIHCGHTFHLOCLIQWFTAPSRPCPCR 47
Db 85 ICCICQDFQRACVGNKLCNGHNFHINSVPMILT--KKQCPVQ 127

RESULT 33
T19328
hypothetical protein Cl6C10.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T19328
R:Ilroy, C.
submitted to the EMBL Data Library, November 1994
A:Reference number: Z19108
A:Accession: T19328
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <NTL>
A:Cross-references: EMBL:Z46787; PIDN:CAA86745.1; GSPDB:GN00021; CESP:Cl6C10.7
A:Experimental source: clone Cl6C10
C:Genetics:
A:Gene: CESP:Cl6C10.7
A:Map position: 3
A:Insertions: 23/2; 105/3; 196/1
C:Superfamily: RING finger homology
F:22-72/Domain: RING finger homology <RRN>

Query Match 33.1%; Score 97; DB 2; Length 235;
Best Local Similarity 40.0%; Pred. No. 0.00032;
Matches 18; Conservative 6; Mismatches 17; Indels 4; Gaps 2;

OY 4 CTICSDFFDHSRDVAAIHCGHTFHLOCLIQWFTAP--SRPCPCR 47

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| | | | : : | | | | : : | | | : : | | :
Db      26 CNIC--LDAAKDAVSLGHLFCMPCLSQMLDPRFNNQVCPVK 67

RESULT 34
996835
Probable RING zinc finger protein, 53384-54880 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96835
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huitzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lutros, J.S.; Mailli, R.; Marzall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: G96835
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-407 <SMD>
C:Genetics:
A:Cross-references: GB:AEO05173; NID:g6751714; PIDN:MAF27696.1; GSDB:GN00141
A:Gene: F516.15
A:Map position: 1

Query Match          33.1%   Score 97; DB 2; Length 407;
Best Local Similarity 33.3%   Pred. No. 0.0005;
Matches 16; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

Oy    4 CTICDFDHSRDVAIHCGHTFHLOCLIQMFETAPSRCTPCCRIOVG 51
      ||||| | | | | | | | | | | | | | | | | | | | |
Db    355 CCICLRTGGDEQVRELPCSHVFYDCVDKMLKT--NATCPCKNEVG 400

RESULT 35
CB5130
hypothetical protein AT4g12190 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C:Accession: CB5130
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488
A:Accession: CB5130
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <SMD>
C:Genetics:
A:Cross-references: GB:NC_001268; NID:g7267920; PIDN:CAB78262.1; GSDB:GN00140
A:Gene: AT4g12190
A:Map position: 4
C:Superfamily: Arabidopsis thaliana hypothetical RING finger protein Fl6J13.210; RING fi

Query Match          32.9%   Score 96.5; DB 2; Length 194;
Best Local Similarity 34.0%   Pred. No. 0.00031;
Matches 17; Conservative 9; Mismatches 19; Indels 5; Gaps 2;

Oy    4 CTICSDFF---DHSRDVAIHCGHTFHLOCLIQMFETAPSRCTPCCRIOVG 50
      ||||| | | | | | | | | | | | | | | | | | | | |
Db    145 CSICLESVSGPKRPDIITRMTCSHVFNHGCCLEWLKR--KNTPCLPRTFL 192

RESULT 36
T48129
hypothetical protein T4c9.30 - Arabidopsis thaliana
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[illegible]

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